8 Predictive Microbiology in Quantitative Risk Assessment

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8.1 INTRODUCTION

Food-borne disease arises from the consumption of microbial pathogens, microbial toxins, or both, by a susceptible individual. The risk of food-borne disease is a combination of the likelihood of exposure to the pathogen, the likelihood of infection or intoxication resulting in illness, and the severity of the illness. In a system as complex as the production and consumption of food, many factors affect both the likelihood and the severity of the occurrence of food-borne disease. Many of these factors are variable and often there are aspects for which little information is currently available. To manage food safety effectively, a systematic means of examining these factors is necessary.

Historically, the production of safe food has been based on numerous codes of practice and regulations enforced by various governing bodies worldwide. With the increased concern regarding the existence of microbial hazards in foods, a more objective approach is warranted, which has led to the introduction of the Hazard

Analysis Critical Control Point (HACCP) system. HACCP as a tool for safety management consists of two processes: building safety into the product and exerting strict process control.[1] The principles of HACCP have been set out by the Codex Alimentarius Commission[2] and consist of seven steps: hazard analysis; determination of critical control points (CCP); specification of criteria; implementation of monitoring system; corrective action; verification; and documentation.[3] HACCP processes as defined for various food products are often based on qualitative information and expert opinion. Moreover, the microbiological criteria underlying HACCP are often poorly understood or defined.[4]

The concept of risk assessment as defined by the Food and Agriculture Organization (FAO) and the World Health Organization (WHO)[5] provides a more quantitative approach to food-borne hazards. Quantitative risk assessment (QRA) is the scientific evaluation of known or potential adverse health effects resulting from human exposure to food-borne hazards.[1,6] Risk assessment is a systematic framework and process that provides an estimate of the probability and impact of food-borne disease. In doing so, exposures to food-borne pathogens are translated into actual human health outcomes.

Quantifying the human health risks associated with the ingestion of specific pathogens in specific foods has been considered feasible only within the last decade. Historically, until the mid-90s, risks associated with foods were estimated, at best, qualitatively, largely with reliance on epidemiological evidence and expert opinion to determine "high risk" vs. "low risk." Evaluations of the risks associated with food-borne hazards, in general or attributable to specific foods, have been predominantly qualitative descriptions of the hazard, routes of exposure, handling practices, consequences of exposure, or all of these. Quantifying any of these elements is challenging, since many factors influence the risk of food-borne disease, complicate interpretations of data about the prevalence, numbers, and behavior of microorganisms, and confound the interpretations of human health statistics. Consequently, policies, regulations, and other types of decisions concerning food safety hazards have been largely based on subjective and speculative information.

Today, advances in our knowledge, analytical techniques, and public health reporting, combined with increased consumer awareness, global trade considerations, and realization of the real economic and social impacts of microbial food-borne illness, have moved us toward the threshold of using QRA to support better prioritizing and decision-making.

Developments in the field of microbial risk assessment have some resemblance to the growth characteristics of a microbial population (see Chapter 2). During what might be termed the lag phase, few researchers attempted to define and model the food chain quantitatively. Today, the field can be described as entering the log phase, as efforts increase internationally to develop sophisticated models in response to risk managers' needs in decision-making.

The recent ratification of the World Trade Organization (WTO) agreement is having a major impact on the development of new approaches for the regulation of food. Countries are encouraged to base their procedures on Codex standards and guidelines to maintain and enhance safety standards.[7] This will lead to the development of harmonized risk assessment and risk management frameworks, providing

input into HACCP, which is the primary vehicle for achieving enhanced food safety goals.[7] As the use of HACCP increases, there will be a need for a clear understanding of the relationship among HACCP, microbiological criteria, and risk assessment.[4] Regulators will be called upon to participate in all aspects of HACCP development, in particular to establish public health-based targets, elucidate microbiological criteria, develop improved techniques in microbiological risk assessment, and develop the means for evaluating the relative performance of HACCP systems.[4] Harmonization of international rules will clearly require standardized approaches.[8]

For microbial pathogens in foods, formal risk assessment has evolved from the traditional fields of application such as toxicology and environmental health risks, but with distinct differences. In particular, survival and/or inactivation of pathogens, and the growth of bacteria, must be accounted for, and assessors require predictive models to estimate these parameters. Second, human responses to microbial pathogens can vary significantly, depending on characteristics of the host's immunity and other defense factors; the pathogen's characteristics and survival and virulence mechanisms; and the characteristics of the food matrix in supporting growth, or in protecting the microorganism from inactivation by processing, or in the human after ingestion. However, the focus of this paper will consider the parameters that are driven in part by our ability to predict exposures.

8.2 ASSESSING MICROBIAL RISKS

There are different approaches that can be taken in microbial risk assessment; however, the basic sections of formal risk assessment are hazard identification, hazard characterization, exposure assessment, and risk characterization.[5,6] These describe, respectively, the nature of the food, the contaminant, and associations with human illness; the characteristics of the disease, the pathogen–host interaction, and if data are available, a mathematical model that quantifies the dose–response relationship; an evaluation of the likely intake of the agent in the food; and an integration of the foregoing information to provide a risk estimate, i.e., the likelihood and severity of the adverse effects in a given population. Risk characterization should also delineate the uncertainties and variability in the data used, and in our understanding of the food system, pathogen behavior and human health response. QRA is also considered to be part of the larger concept of risk analysis, which includes, in addition, risk management and risk communication steps.[9]

QRA and HACCP have some common parameters. Process risk models (see later) may help to identify CCPs and specify where significant risks exist. QRA can have input into specification of criteria for CCPs (step 3 of HACCP), as shown in Figure 8.1.[3] Risk assessment is intended to provide a scientific basis for risk management decisions, while HACCP is a systematic management approach to the control of potential hazards in food operations.[10] Thus, risk assessment concerns the overall product safety, while HACCP enhances overall product safety by assuring day-to-day process control.[10] The view of risk assessment being associated with one step of HACCP may be a limited one; in a contrasting view, both HACCP and risk assessment are encompassed in risk analysis, with HACCP representing one management strategy (Figure 8.1).[10] Nauta[11] has recently clarified this relationship by

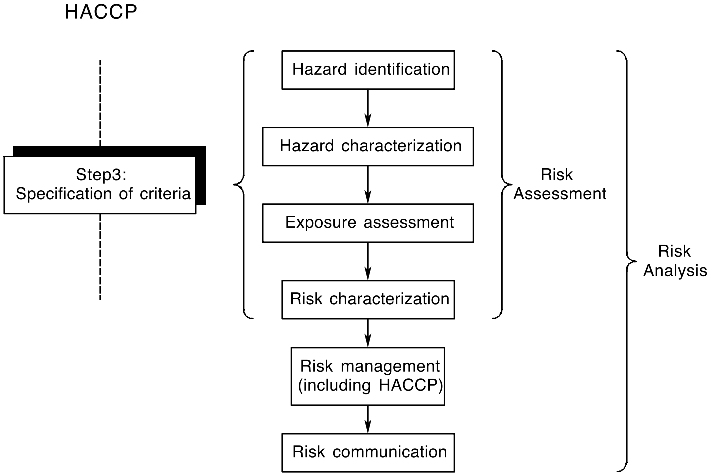


FIGURE 8.1 Relationship among HACCP, quantitative risk assessment, and risk analysis. (Modified from Notermans, S., Gallhoff, G., Zwietering, M.H., and Mead, G.C., *Food Microbiol.*, 12, 81, 1995. With permission.)

stating that while HACCP is typically linked to industrial processes, QRA is used for public health purposes and to help set hazard targets for industry as a whole.

Traditionally, food-borne pathogens and the risk of human illness are often described by descriptive *hazard assessments*, which typically do not actually provide a measure of the risk in terms of likelihood of occurrence and extent of illness (or other endpoint) expected in a population. However, if appropriate, this type of approach can be useful because the information can usually be compiled and summarized quickly if necessary. *Expert knowledge* has also often been relied upon to help decision-makers; however, even experts can misinterpret data, and may be biased towards certain conclusions.

Formal risk assessment based on the four-step framework relies on the basic elements of data, models, and assumptions. The variability and uncertainty in all three elements must be described, either quantitatively or descriptively. The risk assessment must be well documented and transparent; that is, all the data, assumptions, calculations, and technical descriptions should be presented to allow others to understand completely how the conclusions were reached, using what data, and what types of analyses.

We refer to *qualitative* assessments, in which the information used for the assessment is described in general terms, as categories or ratings. For example, ratings of "high," "medium," "low," or "negligible" may be assigned for the various parameters (e.g., pathogen concentration; prevalence, extent of growth/inactivation, or both; amount of food eaten; severity of illness) and for the final risk estimate, based on defined ranges of values for each rating and for each parameter. There are few examples of comprehensive hazard ranking systems. The ICMSF book *Microorganisms in Foods 7: Microbiological Testing in Food Safety Management*[12] gives a good table (in its Chapter 8 appendix) on the ranking of food-borne hazards or

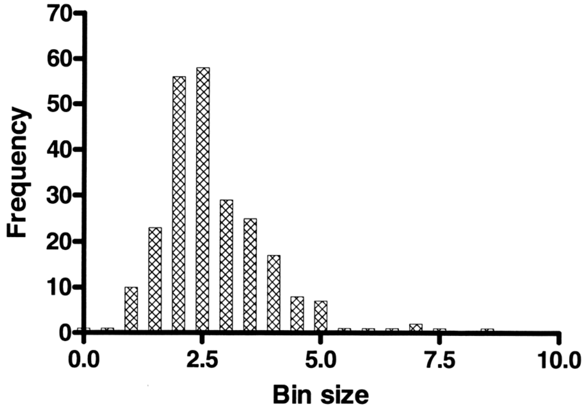


FIGURE 8.2 Example of a log normal distribution.

toxins into hazard groups. In a similar manner, various seafood products have been ranked qualitatively into risk categories.[13]

By contrast, *quantitative risk assessments* require mathematical equations to describe the relationships among all the factors that influence the risk. Quantitative assessments can be point estimates or stochastic (or *probabilistic*). Point-estimate and stochastic models can be differentiated along the lines of their treatment of randomness and probability. Point-estimate models do not include any form of randomness or probability in their characterization of a system, whereas these are fundamental characteristics of probabilistic assessments.

Point-estimate models use a single number for each data set that is used as an input into the model analyzed. For example, the mean concentration (i.e., colony forming units [CFUs] per gram) of *Salmonella* in raw ground beef is a point estimate; the 95th percentile value from a collection of data points would be a "worst-case" point estimate. Probabilistic analyses consider the entire possible range of the numbers of *Salmonella* that may be in the raw product, with the likely frequency at which the various concentrations might occur. Thus, the distribution curve may range from 1.0 to 4.0 logs per gram CFU per gram in product that is positive for the pathogen. Some values will be more likely than others, and this is represented by the height of the distribution curve at those values. This information is derived from one or more sets of laboratory data, or, if few data are available, estimations using sound scientific rationale will be required. The outcome of a point-estimate risk assessment is a single value for the risk estimate, such as 1 in 100,000 probability of illness. A probabilistic risk estimate is a range of values, and how probable each value is likely to be, again depicted by a distribution curve. An example of a lognormal distribution is given in Figure 8.2.

8.3 ROLE OF PREDICTIVE MICROBIOLOGY IN QRA

Most of the risk model development takes place within exposure assessment and dose–response assessment (part of hazard characterization). For some agents, particularly those involving voluntary exposure, such as prescription drugs, exposure

assessment is relatively straightforward. But for other agents, such as environmental or food contaminants, an exposure assessment is usually based on considerable uncertainties. It is often not possible to measure exposures directly; rather they must frequently be predicted, for example, by monitoring data, using mathematical modeling, and reconstructing historical exposure patterns. There are two broad types of mathematical models used in exposure assessment: those that predict probable exposure to the agent and those that predict the probable concentration of the agent. Exposure models can be used to estimate population exposures based on small numbers of representative measurements. Models that predict concentrations can be combined with information on human time–activity patterns to estimate exposures.

Key components of assessing exposures may include:

- The microbial ecology in relation to food
- Intrinsic and extrinsic microbial growth requirements
- Prevalence of infection in food animals
- The initial contamination of the raw materials
- The impact of production, processing, cooking, handling, storing, distribution steps, and preparation by the consumer on the microbial agent
- The variability in processes involved and the level of process control
- Slaughter or harvesting practices and the level of sanitation
- The potential for contamination or recontamination
- The conditions for packaging, distribution, and storage of the food, and the food attributes that could influence growth, toxin production, or both

Implicit in the concept of exposure assessment is the influence of processing and environmental factors on the survival and growth of food-borne pathogens. Mathematical models can predict the extent of impact of unit operations on the numbers of microorganisms, which in turn determines the exposure.[14] Specific mathematical functions to quantitate microbial growth and death can be incorporated into risk assessments.[14–17] For example, the Gompertz function is used to evaluate growth parameters:

$$\log x(t) = A + C\exp\{-\exp[-B(t-M)]\} \tag{8.1}$$

where *x(t)* is the number of cells at time *t*, *A* is the asymptotic count as *t* decreases to 0, *C* is the difference in value of the upper and lower asymptotes, *B* is the relative growth rate at *M*, and *M* is the time when the absolute growth rate is maximum.[18,19]

Thermal death models can be used to establish the *D*-value for a microorganism:

$$\log S_t = -\frac{t}{D} \tag{8.2}$$

where S_t is the survival ratio at time *t*. Much information on microbial growth and survival has been documented, and resulting predictive software such as Food MicroModel has been used to predict the influence of food composition and environmental conditions on growth and survival of potentially hazardous microorganisms.[20] Mod-

els can therefore be used to develop CCPs, and show where data for risk assessments are missing.[21] In addition, models can support regulations and optimize product formulations and support process control.[21] Mathematical modeling can also support quantitation in dose–response assessment. For example, the Beta-Poisson is a commonly used distribution model for dose–response:[14]

$$P_i = 1 - \left(1 + \frac{N}{\beta}\right)^{\alpha} \tag{8.3}$$

where P_i is the probability of infection, N is the exposure, and α and β are coefficients specific to the pathogen.

In QRA, mathematical models are used to estimate the ultimate risk to the consumer as a function of input values taken from various points along the "farm-to-fork" continuum. Because of heterogeneity of microorganisms, variability around single point estimates of risk can be significant. Thus, point estimates give limited information, describing single instances such as worst-case scenarios without any insight into how likely, or unlikely, this is to occur.[14,22] Improvements in prediction can be made by incorporating uncertainty. Uncertainty is an important factor in risk analysis, since failure to account for it limits our ability to make reliable predictions of risk. Uncertainty may arise from inherent variability in the biological system, or from lack of information or understanding of the mechanisms involved.[15] Uncertainty due to lack of information or understanding vs. uncertainty due to variability can sometimes be minimized by obtaining more, high quality data; however, as this is not always feasible, alternatives must be sought. One approach is to use probability distributions to represent parameter values. These distributions can be built from empirical data, knowledge of underlying biological phenomena, or expert opinion.[22] Using distributions as inputs leads to an output where risk is expressed as a probability distribution. Risk analysis software such as @RISK™, which uses Monte Carlo analysis to simulate output distributions of risk on the basis of variability of input data, can facilitate the risk assessment process.[14,22] In Monte Carlo analysis, the point-estimate relations are replaced with probability distributions. Samples are randomly taken from each distribution in a series of iterations, and the results of each iteration are tallied, usually in the form of a probability density function, or cumulative distribution function. This approach yields an output, the risk estimate, that reflects the uncertainty and variability in the data used for the assessment.

As probabilistic models include components of randomness within their definition, these result in outputs that are in fact estimates of the true system. Probabilistic assessments attempt to capture the variability that is naturally present in a biological system. Such models tend to be a better representation of natural systems, given the randomness inherent in nature itself. Clearly, a point-estimate model to describe a natural system is a significant simplification of a biological system; however, with these caveats, a point-estimate model could be entirely appropriate for the problem at hand, and with given resources. What is important is that assessors and managers alike acknowledge the limitations of the information derived from any such risk model.

Nauta[23] has emphasized the need to separate true biological variability (due to heterogeneity of populations) from uncertainty, the lack of perfect knowledge of the parameter values. This is commonly neglected in risk assessment studies. Working with data on growth of *Bacillus cereus* in pasteurized milk, Nauta[23] showed that prediction of outbreak size may depend on the way that uncertainty and variability are separated. Using a deterministic estimate, the exposure assessment model predicted that there was no risk. A stochastic model without separation of uncertainty and variability predicted individual risk, but no major outbreak. In contrast, when uncertainty and variability were differentiated, a potential major outbreak was predicted.

8.4 SCOPE OF RISK ASSESSMENTS

In addition to different modeling approaches, risk assessments can also differ in their scope. In risk ranking, several foods may be compared within the assessment to determine which pose higher or lower risk. This type of assessment is useful for setting priorities for risk management. Farm-to-fork (production-to-consumption) models describe each stage of the food: growing, harvesting, processing, distribution, retail, and preparation pathway. Alternatively, assessments may focus only on the stages after retail distribution. Typically, risk assessments are constructed in a modular sequence of relevant stages in food harvesting/processing/handling/consumption. Submodels within the individual modules, including ones that integrate predictive equations for growth, inactivation, or both, are defined as appropriate. These may be simple or complex equations, reflecting the precision necessary to estimate significant parameters and changes in pathogen number.

8.5 PROCESS RISK MODELING

Evaluating the microbial safety of a food typically requires consideration of multiple factors that influence the prevalence and numbers of a microbial pathogen in the product. As a tool for strategic decision-making, the scope of a risk assessment should include activities that provide relevant information for the risk manager. This approach has been taken for many microbial risk assessments to describe the production-to-consumption pathway. The main goal of such work is to develop a tool that can be used to analyze the relationship between the factors that affect the presence, behavior, and ultimately concentration of microorganisms and the probability of human illness.

The phrase "Process Risk Model" (PRM) has been introduced to describe such risk assessments.[24,25] The basis of a PRM is the mathematical model that predicts the probability of an adverse impact as a function of multiple process parameters. By manipulating the parameters of the sequential stages of food production, the effect of hypothetical risk-reducing strategies that are based upon changing some component of the system is estimated by the changes in the risk prediction under different scenarios. For example, the probabilistic model allows the prediction of a change in a health effect endpoint, such as the expected number of illnesses within

a defined population and time frame, under different HACCP or other types of intervention/control strategies. As a result the model acts as a predictive tool for evaluating future scenarios, rather than presenting a static picture of the present risk to health. Simulation provides this important link between HACCP and QRA.

In addition, intermediate results or outputs from the risk model may be of interest. For example, an intermediate output might be a prediction of the distribution of cell numbers in a package of ground beef, simulated from input parameters of initial carcass contamination, and modeling the changes that occur during slaughter and fabrication. Further analysis of the probabilistic model provides information about key inputs or uncertainties that most significantly influence the risk outcome, thereby identifying potentially effective interventions or research opportunities. Manipulation of the model, by altering input values in "what if" scenarios, can readily provide insight into the effectiveness of proposed risk interventions.[24]

Nauta's[11] modular process risk model (MPRM) constitutes a further improvement on the PRM. In this approach, it is assumed that in any food pathway, all processing steps can be described by six process modules: two microbiological processes (growth or inactivation) and four product handling steps (mixing, partitioning, removal, and cross-contamination). This approach highlighted the importance of including variability in microbial growth models, and provided a tool to identify the most important gaps in knowledge along a food pathway.

8.6 EXAMPLES OF RISK MODELING

There have been very few examples of well-developed QRA for specific microbial hazards in foods. Much of the work published to date is about quantitative models that describe either exposure or dose–response relationships. Schlundt[26] reviewed several microbial risk assessments published between 1996 and 1998 with a view to assessing the state of the art. He noted that few of the studies comprised a full Codex–based risk assessment.[6] Often the purpose of these studies did not relate directly to risk analysis, and the factors that determined the risk were not identified. The driving force for many of these studies was the use and application of mathematical models; thus the focus was largely on exposure assessment. Examples of some recently published food safety assessments are given in Table 8.1.

One of the important developments in QRA is the establishment of risk assessment simulations that can be easily accessed by users. A few examples of these follow. Oscar[27] has developed an interactive Microsoft® Excel-based spreadsheet called Poultry Farm Assess Risk Model (Poultry FARM). This model uses the risk analysis software @RISK™ to provide poultry companies and regulatory agencies with the tools they need to make informed public health decisions. van Gerwen et al.[28] have described a system for microbiological QRA of a cheese spread. Predictive models were incorporated with a decision support expert system called SIEFE: Stepwise and Interactive Evaluation of Food Safety by an Expert System. This approach combined quantitative information on the production processes with qualitative expert knowledge expressed as a series of rules. Ross and Sumner[29] have also developed a Microsoft Excel spreadsheet model for QRA. In this model,

TABLE 8.1
Examples of Currently Published Microbial Food Safety Exposure, Dose–Response, and Risk Assessments

Microorganism	Commodity	Type of Assessment	Reference
Bacillus cereus	Pasteurized milk	Semiquantitative, from retail to consumer	33
	Chinese-style rice	Probabilistic risk estimation, raw product to consumer	34
	Vegetable puree	Exposure assessment, retail to consumer	35
B. cereus, C. perfringens	Cooked chilled vegetables	Probabilistic exposure assessment, product preparation and storage	36
Listeria monocytogenes	Pasteurized milk	Point-estimate hazard/exposure assessment	37
	Pâté and soft cheese	Quantitative (simple), retail to consumer	38
	Ready-to-eat meat and smoked fish	Quantitative dose–response assessment	39
	Raw milk soft cheese	Probabilistic risk estimation, from farm to consumer	38
	Smoked or gravad fish	Quantitative, from retail to consumer	40
	Ready-to-eat foods	Probabilistic risk ranking	41
Salmonella Enteritidis	Cracked eggs	Semiquantitative, from eggs to consumer	42
	Pasteurized liquid egg	Probabilistic risk estimation, from eggs to consumer	43
	Shell eggs	Probabilistic risk estimation, from farm to consumer	31 44, 45
Salmonella spp.	Poultry and products	Probabilistic risk estimation from processing to consumer	27, 31, 46
Mycobacterium paratuberculosis	Pasteurized milk	Probabilistic vs. point-estimate exposure assessments	47
Escherichia coli O157:H7	Ground beef	Probabilistic risk estimation, from cattle to consumer	25, 48
		Probabilistic risk estimation, retail to consumer	49
	Raw fermented sausage	Probabilistic exposure assessment, cattle to retail	50

qualitative inputs are converted into numerical values, and then combined with quantitative inputs in a series of mathematical and logical steps. It was designed as a generic model, to give a quick and simple means of comparing food-borne risks from diverse products.

There are different approaches to risk modeling; thus it is appropriate to discuss here some illustrative examples in more detail. The PRM for *Escherichia coli* O157:H7 in ground beef reported by Cassin et al.[25] is one of the best developed and most detailed models available. The PRM is limited to a particular food production system, and predicts the distribution of probability of illness attributable to *E. coli*

O157:H7 in a particular ground beef scenario.[25] In contrast, the Poultry FARM model described by Oscar[27] is a packaging-to-consumption model that assesses the risk and severity of *Salmonella* spp. and *Campylobacter jejuni* infections from chicken. Outputs include the concentrations of pathogens at each stage of the process, and the health outcome assessment, which takes into account the number of patients who might seek medical treatment, and suffer death or chronic sequelae.

8.6.1 PRM FOR *E. COLI* O157:H7 IN GROUND BEEF

The model of Cassin et al.[25] describes the probability of becoming ill with *E. coli* O157:H7 as a result of consuming undercooked ground beef. It models the production of beef trimmings by a hypothetical abattoir, which are subsequently ground and sold by retailers. Figure 8.3 shows the flow diagram of the process. *E. coli* O157:H7 is the primary microbial hazard identified with ground beef. Cattle are known to be a reservoir for this pathogen, which is shed in feces, and can then subsequently contaminate the carcass during slaughter. *E. coli* O157:H7 is a human pathogen that can cause severe infection, often resulting in death or permanent damage. There have been a number of food-borne outbreaks attributed to undercooked ground beef.

As mentioned earlier, exposure assessment is one of the most important aspects of QRA. In this step, the potential exposure to the pathogen was determined in a single-serving meal. In this model, multiple stages of product handling were described, with appropriate probability distributions assigned to each step, based on available data. The various stages include production; processing and grinding; postprocessing conditions such as microbial growth and thermal inactivation; and consumption.

The production stage concerns the potential concentration of fecal material on the beef carcass. This depends on the level of *E. coli* O157:H7 in feces, which is affected by many factors including season, age of animal, and feeding practices. Prevalence relates to the relative number of animals that shed the pathogen, both within and between herds. Processing includes skinning, evisceration, and trimming. During the skinning process, fecal material from the hide can contaminate the carcass. Previous studies have shown that the various decontamination steps such as trimming of visible contamination and washing using a variety of methods have limited effect on the level of contamination. During the subsequent chilling of the carcass, some microbial growth can occur.

Trimmings collected during the deboning stage are then combined into 5-kg lots, and sent to retailers for grinding. During storage of the ground beef, some microbial growth can occur, and this can be modeled using common functions such as the Gompertz equation (see Chapter 2). The effect of temperature can be modeled using Food MicroModel (see Chapter 6). Finally, cooking is the most effective barrier against *E. coli* O157:H7 exposure, and modeling was based on the cooking preference of the consumer.

A dose–response model based on the Beta-Poisson model was constructed. It was assumed that the virulence of the pathogen is similar to that of *Shigella dysenteriae*, and model parameters were selected based on human feeding studies. The

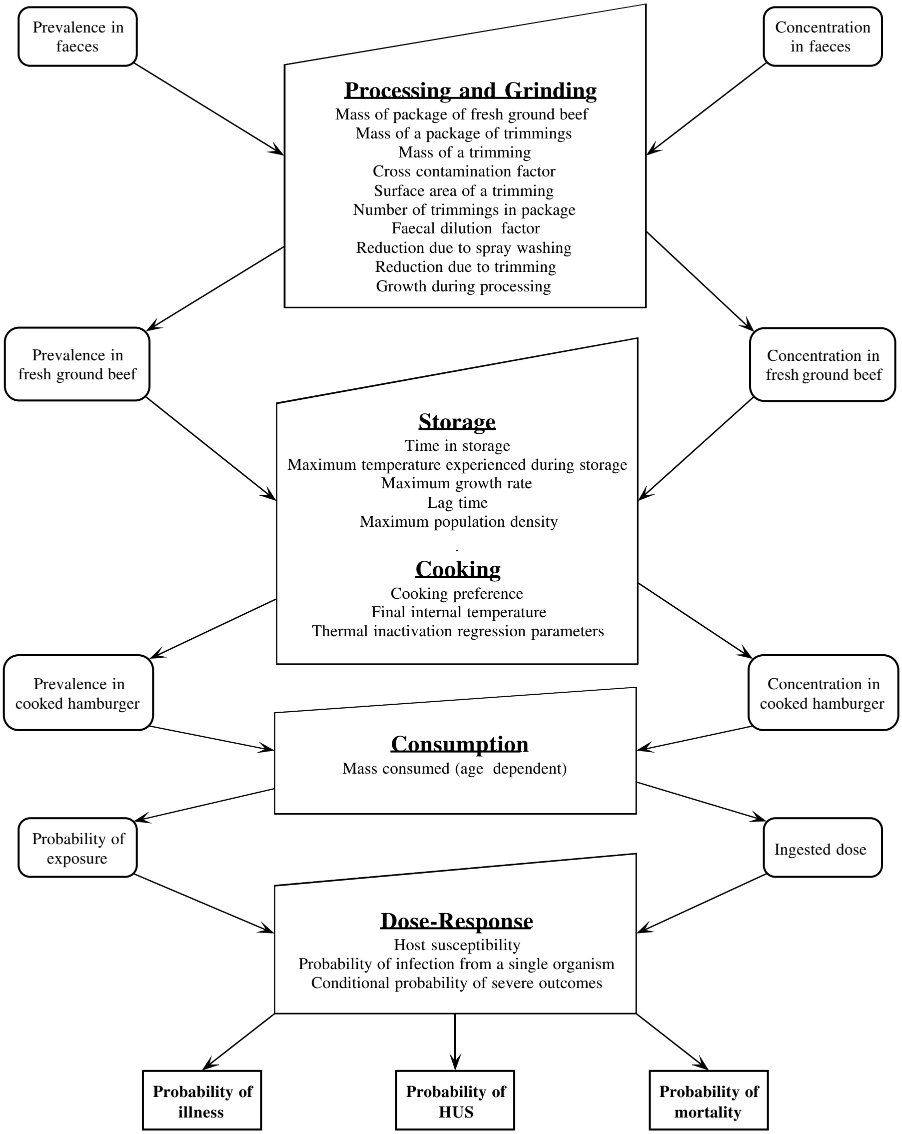


FIGURE 8.3 Flow diagram of the mathematical model of exposure assessment and dose–response for *E. coli* O157:H7 in hamburgers. (From Cassin, M.H., Lammerding, A.M., Todd, E.C.D., Ross, W., and McColl, R.S., *Int. J. Food Microbiol.*, 41, 21, 1998. With permission.)

dose–response curve for an adult population is shown in Figure 8.4. The susceptible population, i.e., young children, was assumed to have a similar vulnerability, but an increased propensity for more severe outcomes. As a final step in development of the model, the probability of illness was the product of the probability of a nonzero exposure and the output of the dose–response model.

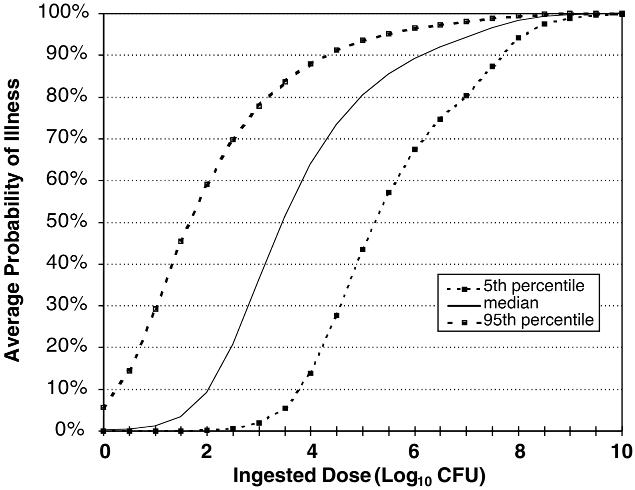


FIGURE 8.4 Beta-Binomial dose–response model — uncertainty in average probability of illness vs. ingested dose of *E. coli* O157:H7. (From Cassin, M.H., Lammerding, A.M., Todd, E.C.D., Ross, W., and McColl, R.S., *Int. J. Food Microbiol.*, 41, 21, 1998. With permission.)

A simulated distribution of probability of illness per meal is shown in Figure 8.5. It is not a simple matter to determine the risk of a specific health outcome, since a wide range of scenarios can exist. The risk for most scenarios is less than 1 in 10,000 (Figure 8.5). The expected value of risk was also calculated, which is a point estimate of the probability of a particular health effect occurring. This value is often used to compare with regulatory objectives to meet standards of acceptable risk; however, the range of risk experienced by the population is lost.

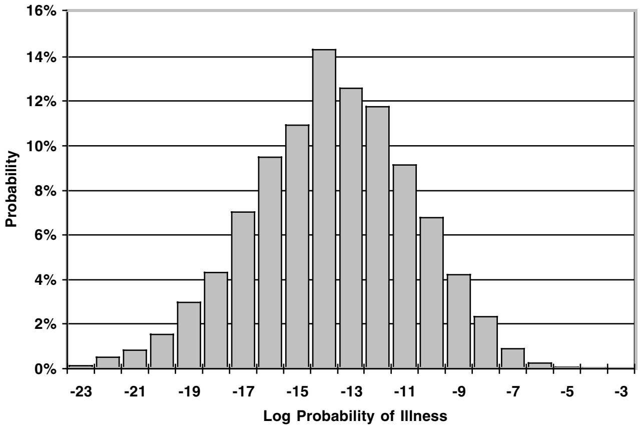


FIGURE 8.5 Probability distribution for probability of illness from a single hamburger meal predicted by the *E. coli* O157:H7 Process Risk Model (PRM). (From Cassin, M.H., Lammerding, A.M., Todd, E.C.D., Ross, W., and McColl, R.S., *Int. J. Food Microbiol.*, 41, 21, 1998. With permission.)

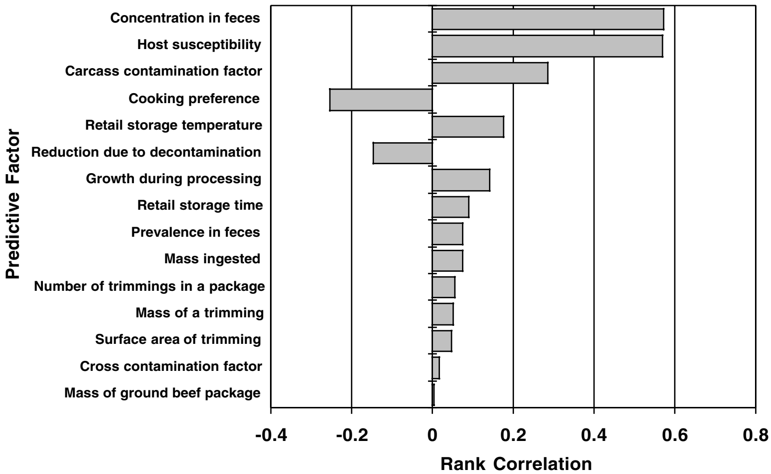


FIGURE 8.6 Spearman rank correlation between the estimated probability of illness and the 15 most important predictive factors of the Process Risk Model (PRM). (From Cassin, M.H., Lammerding, A.M., Todd, E.C.D., Ross, W., and McColl, R.S., *Int. J. Food Microbiol.*, 41, 21, 1998. With permission.)

CCPs can be identified from a PRM using importance analysis. Importance analysis includes the sensitivity of the outcome to a factor, and the uncertainty and variability of that factor. The Spearman rank correlation coefficient was used to measure importance, and a tornado graph showing the 15 predicting factors most highly correlated with risk is shown in Figure 8.6. The concentration of *E. coli* O157:H7 in the feces was the most highly correlated factor, which points out the importance of animal prescreening prior to slaughter, or some intervention that reduces numbers in the feces of the live animal. Host susceptibility (probability of illness from a single organism), carcass contamination factor (relationship between concentration in the feces and on the carcass), and cooking preference were also important risk factors.

The ability to propose appropriate risk mitigation strategies is an important outcome of a PRM. Hypothetical strategies such as improvements in storage temperature, better preslaughter screening, and institution of a consumer information program were simulated using the *E. coli* O157:H7 PRM. These were defined to have an assumed level of compliance with the intervention. It was found that reducing the average temperature of storage at the retail level from 10 to 8°C, with the maximum expected of 13 instead of 15°C, reduced the risk of illness by 80%. In contrast, the effectiveness of consumer education on the importance of fully cooking hamburgers was predicted to reduce risk by only 16%.

8.6.2 Poultry Farm Model

This model predicts the change in concentration of *Salmonella* spp. or *C. jejuni* in a single serving of chicken from packaging at the processing plant, through to consumption by the consumer, as well as adverse health outcomes. It is structured as one simulation model (using @RISK in a Microsoft® Excel spreadsheet) and four

TABLE 8.2
Simulation Conditions for Poultry FARM Model Describing the Fate of *Salmonella* spp. on Chicken from Production to Consumption

Node	Incidence (%)	Extent[a]		
		Minimum	Most Likely	Maximum
Packaging	20	0.0	2.5	4.5
Cold storage	100	–2.0	–0.3	0.0
Distribution	40	0.0	0.3	3.0
Cooking	15	–9.0	–6.0	0.0
Cooling	20	0.0%	0.1%	0.5%
Consumption	20	0.0	0.2	2.0
Infection		1.3	3.3	8.3

[a] Units are: Packaging, log number/serving; Cold Storage, Distribution, Cooling, Consumption (log change/serving); Cooling (% transfer/serving); Infection (log number).

predictive models. In this example, we will address the prediction of only *Salmonella* spp. during the process.

The various nodes described in the model are given in Table 8.2. At each stage, the change in numbers per serving is calculated by drawing a value from the given extent, ranging from the minimum to the maximum expected value, with an intermediate value representing the most likely outcome. The value for incidence is used to specify the number of servings predicted to be contaminated with *Salmonella* e.g., 20% of 100,000, or 20,000 (Table 8.2). During cold storage, the numbers are expected to decrease by a minimum of –2.0, a maximum of 0.0, and a most likely value of –0.3 log cfu per serving in 100% of the servings (Table 8.2).

The other nodes work in a similar fashion. The incidence value in the cooking node represents the 15% of consumers who are expected to undercook their chicken, and during cooling, it is expected that 20% of consumers will expose the cooked chicken to temperature abuse. Changes in the *Salmonella* content of each serving of the chicken were accumulated over the whole process, and infection was expected to occur if the cumulative numbers exceeded the minimum infective dose. This calculation assumed that one *Salmonella* was capable of causing an infection, and that resulted in 100% probability of developing salmonellosis. This calculation is similar to an exponential dose–response model.

Health outcomes were further calculated from the infection incidence. It was assumed that 45.4% of those infected became sick, that 20.7% of infected victims visited a doctor, 4.1% were admitted to hospital, 2.3% experienced chronic sequelae, and 0.1% died.[30]

The @RISK model was simulated 100,000 times to represent the number of servings being considered, and the outputs are given in Figure 8.7 and Figure 8.8. In Figure 8.7, the exposure assessment is presented as the change in log number of

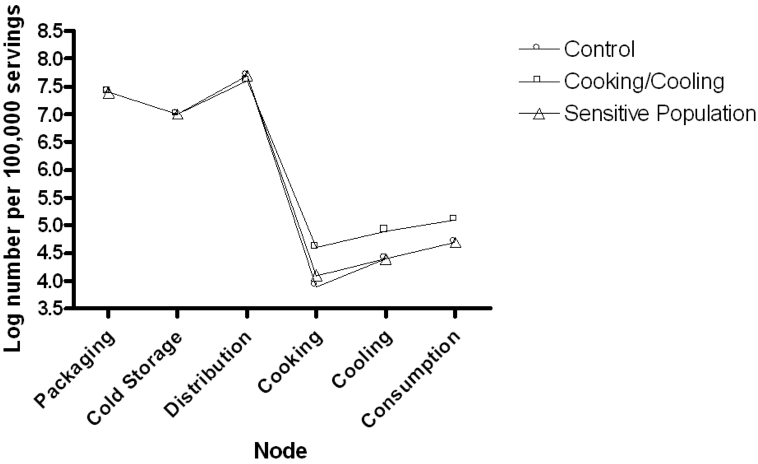


FIGURE 8.7 Exposure assessment for *Salmonella* spp. on chicken for the Poultry FARM model of Oscar.[27]

Salmonella per 100,000 servings over the whole process. In Figure 8.8, the health outcome assessment is given as number of cases per 100,000 consumers. When the simulation was performed using the values given in Table 8.2, the exposure assessment (Figure 8.7; control) showed that the cooking step had the greatest impact on numbers of *Salmonella*. Under these conditions, the number of consumers infected was 43 out of 100,000, with <0.1 deaths (Figure 8.8).

The simulation was repeated with changes made in the initial assumptions. To simulate cases of abuse, it was assumed that the proportion of consumers undercooking their chicken was 75% rather than 15%, and the proportion of consumers exposing the cooked chicken to temperature abuse during cooling was 75% rather than 20%. In the exposure assessment (Figure 8.7), the combined abuse treatments resulted in an increase of 0.5 log numbers by the end of the cooling step. This translated into an increase in infections to 138 per 100,000 consumers, with a 0.14 death rate (Figure 8.8). In a further example, the incidence of cooking or cooling abuse was kept the same as in the control, and the influence of exposure to a more susceptible population was simulated. This was achieved by decreasing the assumed infection level (minimum, most likely, and maximum) by 1 log. The results of this simulation showed that, as expected, this change did not influence the exposure assessment (Figure 8.7); however, the infection rate increased to 168 per 100,000, and the death rate to 0.17 (Figure 8.8). With other simulations based on predicted changes in processing or consumption patterns, it would be possible to determine those factors that have the greatest impact on health outcomes.

8.7 MODIFYING RISK: CONCENTRATION VS. PREVALENCE

In addition to identifying and quantitating risks, risk assessments can also provide information on the relative impact of intervention strategies. The number of

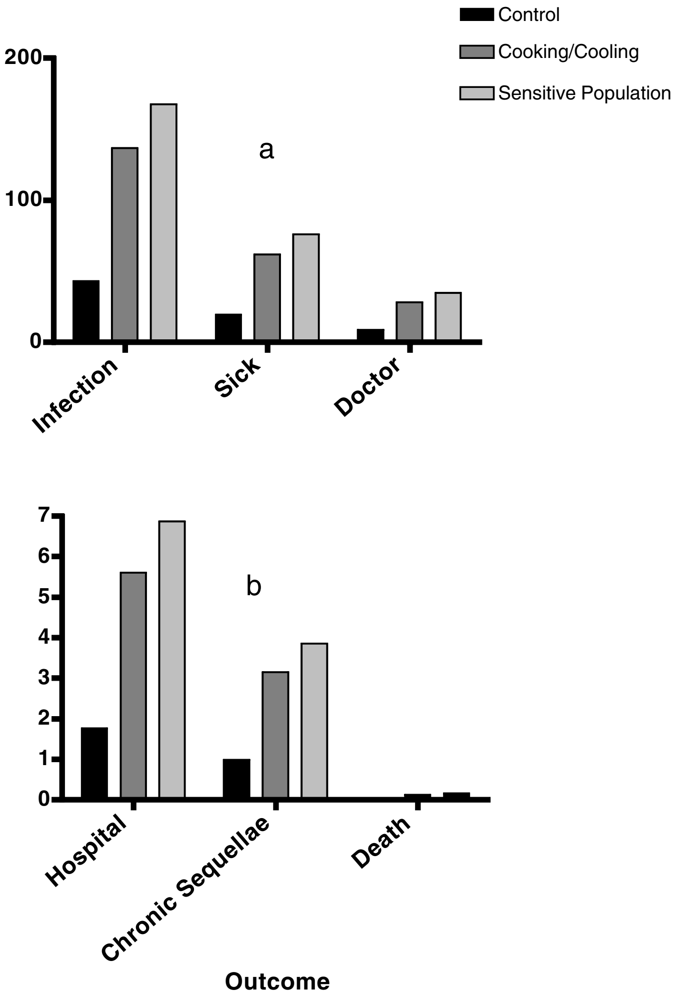


FIGURE 8.8 Health outcome assessment for *Salmonella* spp. on chicken for the Poultry FARM model of Oscar.[27]

microorganisms present in a sample of raw food has a direct impact on the number finally consumed; however, initial numbers may be influenced by either concentration (number per unit weight) or prevalence (proportion of units contaminated). This can be demonstrated by reference to data used for a FAO/WHO risk assessment on *Salmonella* in broiler chickens.[31] In this study, the prevalence of *Salmonella* was determined after immersion in the chill tank with and without chlorine. Data show that carcass cross-contamination was significantly reduced by inclusion of chlorine. Reducing prevalence of *Salmonella*-contaminated carcasses was estimated to have a one-to-one effect on risk reduction.

The effects of reducing the numbers of *Salmonella* on poultry carcasses without changing the prevalence of contaminated carcasses was also assessed using the risk

assessment model. A change in concentration does not necessarily have a linear relationship with risk outcome, as is found for prevalence. Assuming a constant prevalence of 20%, and reducing the concentration, gave a reduction in illnesses per million servings from 11.3 to 4.28.[31] However, these observations pertain to individual units that will be prepared by a consumer vs. raw material units that would be comingled during processing and before consumption.

8.8 WHAT IS THE RIGHT MODEL TO USE?

Clearly, there are many options available to microbial risk assessors, from simple descriptive evaluations to highly complex and detailed analyses. In reality, a combination of techniques and analyses will often be incorporated into a single assessment, for example, qualitative information, expert knowledge, and quantitative analyses of available data, when appropriate. The decision of what approach to use, what analytical techniques are needed, and the scope and level of detail of the assessment will be dependent on the nature of the risk management question, and practical issues such as time, expertise, and other resources that are needed. In international trade disputes, the demands are for quantitative microbial risk assessments with some measure of variability and uncertainty. At the national level, the urgency and nature of the risk issue will dictate what approach is needed.

Microbiological models to predict pathogen growth, survival, or inactivation can differ in mathematical complexity, but a complex model may not necessarily be the best choice to answer a particular risk management question.[28] The need for an accurate prediction needs to be offset by consideration of whether the model is easy to use, whether it is robust and precise, and whether it has been validated against independent data. For example, if the objective of a risk assessment is to identify the most significant risk factors in a process, a simple model may have advantages over a complex model. However, if an accurate prediction of bacterial numbers is necessary, a more complex and accurate model may be preferable. In the choice of a suitable model, one must also consider the quality of data that are going to be used to generate a prediction. If the temperature data on a process are poor, it may not be appropriate to use a complex model for the predictions. Often, this can lead to a misinterpretation of the accuracy of the final prediction. The most appropriate model would be the simplest model possible for a given purpose and the given data quality, provided that it is validated and precise. A good model should also be subjected to an analysis that quantifies the accuracy and bias of its predictions.[32] Ideally, a model should be both accurate and unbiased. Models in risk assessment must adequately reflect reality.

8.9 FUTURE DIRECTIONS

At the present time, microbial risk assessors acknowledge many limitations in providing exact estimates of risk, and in the elements of any one risk assessment: the data available, the models developed to describe both the physical and mathematical aspects, and the assumptions necessary to construct these assessments.

Validating the outcomes of a risk assessment also provides a challenge; in many cases, any and all available data for a particular food/pathogen combination are used for assessing exposures and dose–response relations. This leaves a risk estimate, or intermediate outputs, that cannot be validated against independent data.

An additional challenge will be to facilitate the incorporation of existing and new mathematical models into the QRA framework. Many potentially useful models have been developed and published; however, these often exist independent of the specific needs of the regulators and the food industry. There is no definitive process by which these models can be combined with expert opinion and knowledge and other data on (for example) prevalence to clearly and unequivocally define the risk of consumption of a particular food. Some mathematical model databases exist, but these seldom describe the stochastic aspects of the underlying data. It is clear that in future researchers must work closely with regulators and the industry to improve the technology transfer.

8.10 CONCLUSIONS

Currently, there are many aspects of microbial contamination of foods, and the human health responses to pathogens, for which there are few data. However, the development of even preliminary quantitative risk models in a systematic way will help to identify what critical information is lacking, and help to guide future data gathering efforts. Finally, it is worth recognizing that risk assessment models should be considered "dynamic." As modeling tools improve, better data become available, and as we learn more about pathogen–food–host relationships and microbial responses, risk models will be updated and refined to provide better risk estimates. One continuing challenge will be to make sure that QRA models are kept current, so that they continue to be relevant to the changing needs of the food industry. The process of QRA is still in its infancy, however, and standards have yet to be developed. There is a clear advantage to the food industry and consumers to further develop the concepts of QRA and apply them to both common and novel food processes, and it is expected that significant advances will be made in this field over the next decade.

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